CLAIMS

5

10

15

20

What is claimed is:

- 1. An isolated nucleic acid molecule comprising:
 - a) a nucleic acid having a nucleotide sequence which encodes an amino acid sequence exhibiting at least 40% sequence identity to an amino acid sequence encoded by
 - (1) a nucleotide sequence described in REF and/or SEQ Tables 1 and/or 2 or a fragment thereof; or
 - (2) a complement of a nucleotide sequence shown in REF and/or SEQ Tables 1 and/or 2 or a fragment thereof;
 - b) a nucleic acid which is the reverse of the nucleotide sequence according to subparagraph (a), such that the reverse nucleotide sequence has a sequence order which is the reverse of the sequence order of the nucleotide sequence according to subparagraph (a);
 - c) a nucleic acid capable of hybridizing to a nucleic acid having a sequence selected from the group consisting of:
 - (1) a nucleotide sequence which is shown in REF and/or SEQ Tables 1 and/or 2; and
 - (2) a nucleotide sequence which is complementary to a nucleotide sequence shown in REF and/or SEQ Tables 1 and/or 2, under conditions that permit formation of a nucleic acid duplex at a temperature from about 40°C and 48°C below the melting temperature of the nucleic acid duplex;

with the proviso that said sequence a), b), or c) is not any of the sequences described in the Tables of any of Patent Publication Nos. WO200040695, CA2300692 A1, EP1033405 A2, CA2302828A1 and EP1059354 A2.

- 2. An isolated nucleic acid molecule comprising a nucleic acid having a nucleotide sequence which exhibits at least 65% sequence identity to
 - a) a nucleotide sequence shown in REF and/or SEQ Tables 1 and/or 2 or a fragment thereof; or
- b) a complement of a nucleotide sequence described in REF and/or SEQ Tables 1 and/or 2 or a fragment thereof;

with the proviso that said sequence a) or b) is not any of the sequences described in the Tables of any of Patent Publication Nos. WO200040695, CA2300692 A1, EP1033405 A2, CA2302828A1 and EP1059354 A2.

- 3. The nucleic acid molecule according to claim 1, wherein said nucleic acid comprises an open reading frame.
- 4. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid is capable of functioning as a promoter, a 3' end termination sequence, an untranslated region (UTR), or as a regulatory sequence.
- 5. The isolated nucleic acid molecule of claim 4, wherein (a) when said nucleic acid is a promoter it comprises a sequence selected from the group consisting of a TATA box sequence, a CAAT box sequence, a motif of GCAATCG or any transcription-factor binding sequence, and any combination thereof; and (b) when said nucleic acid sequence is a regulatory sequence it is capable of promoting seed-specific expression, embryo-specific expression, ovule-specific expression, tapetum-specific expression or root-specific expression of a sequence or any combination thereof.
- 6. A vector construct comprising:

5

5

- a) a first nucleic acid having a regulatory sequence capable of causing transcription and/or translation; and
- b) a second nucleic acid having the sequence of the isolated nucleic acid molecule according to claim 1;

wherein said first and second nucleic acids are operably linked and wherein said second nucleic acid is heterologous to any element in said vector construct.

- 7. The vector construct according to claim 6, wherein said first nucleic acid is native to said second nucleic acid.
- 8. The vector construct according to claim 6, wherein said first nucleic acid is heterologous to said second nucleic acid.
- 9. A host cell comprising an isolated nucleic acid molecule according to claim 1, wherein said nucleic acid molecule is flanked by exogenous sequence.
- 10. A host cell comprising a vector construct of claim 6.
- 11. An isolated polypeptide comprising an amino acid sequence

10

5

- a) exhibiting at least 40%, or 75%, or 85%, or 90% sequence identity of an amino acid sequence encoded by a sequence shown in REF and/or SEQ Tables 1 and/or 2 or a fragment thereof; and
- b) capable of exhibiting at least one of the biological activities of the polypeptide encoded by said nucleotide sequence shown in REF and/or SEQ Tables 1 and/or 2 or a fragment thereof;

with the proviso that said sequence a) or b) is not any of the sequences described in the Tables of any of Patent Publication Nos. WO200040695, CA2300692 A1, EP1033405 A2, CA2302828A1 and EP1059354 A2.

- 12. An antibody capable of binding the isolated polypeptide of claim 11.
- 13. A method of introducing an isolated nucleic acid into a host cell comprising:
 - a) providing an isolated nucleic acid molecule according to claim 1; and
 - b) contacting said isolated nucleic with said host cell under conditions that permit insertion of said nucleic acid into said host cell.
- 14. A method of transforming a host cell which comprises contacting a host cell with a vector construct according to claim 6.
- 15. A method of modulating transcription and/or translation of a nucleic acid in a host cell comprising:
 - a) providing the host cell of claim 9; and
 - b) culturing said host cell under conditions that permit transcription or translation.
- 16. A method for detecting a nucleic acid in a sample which comprises:
 - a) providing an isolated nucleic acid molecule according to claim 1;
 - contacting said isolated nucleic acid molecule with a sample under conditions which permit a comparison of the sequence of said isolated nucleic acid molecule with the sequence of DNA in said sample; and
 - c) analyzing the result of said comparison.
- 17. A plant or cell of a plant which comprises a nucleic acid molecule according to claim 1 which is exogenous or heterologous to said plant or plant cell.
- 18. A plant or cell of a plant which comprises a vector construct according to claim 6.
- 19. A plant which has been regenerated from a plant cell according to claim 17.
- 20. A plant which has been regenerated from a plant cell according to claim 18.

SCHEMATIC 1

SCHEMATIC OF A GENE

2

Terminal	- >	· -	Poly A Signal	3.UTR	tion of	
			Intron	Coding Region 3'	fs that specific DNA conformation, chromatin conformation, extent and position of base methylation and biding sites of proteins that control of these.	
Translational Start Site 	V	Facility	Transcription I Start Site	5.UTR	conformation, chro biding sites of pr	Gene
TATA	- >		ŢŢ		ecific DNA lation and D	
Transcription factor Binding sites anscription CAAT		- <	 Enhancer 2	Promoter	Sequences/motifs that specifi base methylatio	
Transcripti Binding : Transcription 10 l		5	Enhancer 1		25 Sequence	
		-	(7)		(1)	